

## SEQUENCE LISTING

&lt;110&gt; SOLVAY PHARMACEUTICALS B.V.

&lt;120&gt; Novel human G-protein coupled receptor

&lt;130&gt; SPW99.04

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 18

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1659

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (36)..(1559)

&lt;400&gt; 1

gcctgcaacc tgtcycacgc cctctggctg ttgcc atg acg tcc acc tgc acc 53  
 Met Thr Ser Thr Cys Thr  
 1 5

aac agc acg cgc gag agt aac agc agc cac acg tgc atg ccc ctc tcc 101  
 Asn Ser Thr Arg Glu Ser Asn Ser Ser His Thr Cys Met Pro Leu Ser  
 10 15 20

aaa atg ccc atc agc ctg gcc cac ggc atc atc cgc tca acc gtg ctg 149  
 Lys Met Pro Ile Ser Leu Ala His Gly Ile Ile Arg Ser Thr Val Leu  
 25 30 35

gtt atc ttc ctc gcc gcc tct ttc gtc ggc aac ata gtg ctg gcg cta 197  
 Val Ile Phe Leu Ala Ala Ser Phe Val Gly Asn Ile Val Leu Ala Leu  
 40 45 50

gtg ttg cag cgc aag ccg cag ctg ctg cag gtg acc aac cgt ttt atc 245  
 Val Leu Gln Arg Lys Pro Gln Leu Leu Gln Val Thr Asn Arg Phe Ile  
 55 60 65 70

ttt aac ctc ctc gtc acc gac ctg ctg cag att tcg ctc gtg gcc ccc 293  
 Phe Asn Leu Leu Val Thr Asp Leu Leu Gln Ile Ser Leu Val Ala Pro  
 75 80 85

tgg gtg gtg gcc acc tct gtg cct ctc ttc tgg ccc ctc aac agc cac 341  
 Trp Val Val Ala Thr Ser Val Pro Leu Phe Trp Pro Leu Asn Ser His  
 90 95 100

ttc tgc acg gcc ctg gtt agc ctc acc cac ctg ttc gcc ttc gcc agc 389  
 Phe Cys Thr Ala Leu Val Ser Leu Thr His Leu Phe Ala Phe Ala Ser  
 105 110 115

24  
 1003049.0140

at  
cont

Gln Cys Ser Ile Asp Leu Gly Glu Asp Gly Met Glu Phe Gly Glu Asp  
345 350 355

gac atc aat ttc agt gag gat gac gtc gag gca gtg aac atc ccg gag 1157  
Asp Ile Asn Phe Ser Glu Asp Asp Val Glu Ala Val Asn Ile Pro Glu  
360 365 370

agc ctc cca ccc agt cgt cgt aac agc aac agc aac cct cct ctg ccc 1205  
Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn Ser Asn Pro Pro Leu Pro  
375 380 385 390

agg tgc tac cag tgc aaa gct gct aaa gtg atc ttc atc atc att ttc 1253  
Arg Cys Tyr Gln Cys Lys Ala Ala Lys Val Ile Phe Ile Ile Ile Phe  
395 400 405

tcc tat gtg cta tcc ctg ggg ccc tac tgc ttt tta gca gtc ctg gcc 1301  
Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys Phe Leu Ala Val Leu Ala  
410 415 420

gtg tgg gtg gat gtc gaa acc cag gta ccc cag tgg gtg atc acc ata 1349  
Val Trp Val Asp Val Glu Thr Gln Val Pro Gln Trp Val Ile Thr Ile  
425 430 435

atc atc tgg ctt ttc ttc ctg cag tgc tgc atc cac ccc tat gtc tat 1397  
Ile Ile Trp Leu Phe Phe Leu Gln Cys Cys Ile His Pro Tyr Val Tyr  
440 445 450

ggc tac atg cac aag acc att aag aag gaa atc cag gac atg ctg aag 1445  
Gly Tyr Met His Lys Thr Ile Lys Lys Glu Ile Gln Asp Met Leu Lys  
455 460 465 470

aag ttc ttc tgc aag gaa aag ccc ccg aaa gaa gat agc cac cca gac 1493  
Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys Glu Asp Ser His Pro Asp  
475 480 485

ctg ccc gga aca gag ggt ggg act gaa ggc aag att gtc cct tcc tac 1541  
Leu Pro Gly Thr Glu Gly Gly Thr Glu Gly Lys Ile Val Pro Ser Tyr  
490 495 500

gat tct gct act ttt cct tgaagttagt tctaaggcaa accttgaaaa 1589  
Asp Ser Ala Thr Phe Pro  
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tcagtccttc agccacagct atttagagct ttaaaactac caggttcaat cactggttat 1649

gctttctgtg 1659

<210> 2  
<211> 508  
<212> PRT  
<213> Homo sapiens

<400> 2  
Met Thr Ser Thr Cys Thr Asn Ser Thr Arg Glu Ser Asn Ser Ser His  
1 5 10 15

A4 Cont

Thr Cys Met Pro Leu Ser Lys Met Pro Ile Ser Leu Ala His Gly Ile  
 20 25 30  
 Ile Arg Ser Thr Val Leu Val Ile Phe Leu Ala Ala Ser Phe Val Gly  
 35 40 45  
 Asn Ile Val Leu Ala Leu Val Leu Gln Arg Lys Pro Gln Leu Leu Gln  
 50 55 60  
 Val Thr Asn Arg Phe Ile Phe Asn Leu Leu Val Thr Asp Leu Leu Gln  
 65 70 75 80  
 Ile Ser Leu Val Ala Pro Trp Val Val Ala Thr Ser Val Pro Leu Phe  
 85 90 95  
 Trp Pro Leu Asn Ser His Phe Cys Thr Ala Leu Val Ser Leu Thr His  
 100 105 110  
 Leu Phe Ala Phe Ala Ser Val Asn Thr Ile Val Leu Val Ser Val Asp  
 115 120 125  
 Arg Tyr Leu Ser Ile Ile His Pro Leu Ser Tyr Pro Ser Lys Met Thr  
 130 135 140  
 Gln Arg Arg Gly Tyr Leu Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile  
 145 150 155 160  
 Leu Gln Ser Thr Pro Pro Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp  
 165 170 175  
 Glu Arg Asn Ala Leu Cys Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr  
 180 185 190  
 Thr Ile Leu Ser Val Val Ser Phe Ile Val Ile Pro Leu Ile Val Met  
 195 200 205  
 Ile Ala Cys Tyr Ser Val Val Phe Cys Ala Ala Arg Arg Gln His Ala  
 210 215 220  
 Leu Leu Tyr Asn Val Lys Arg His Ser Leu Glu Val Arg Val Lys Asp  
 225 230 235 240  
 Cys Val Glu Asn Glu Asp Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe  
 245 250 255  
 Gln Asp Glu Ser Glu Phe Arg Arg Gln His Glu Gly Glu Val Lys Ala  
 260 265 270  
 Lys Glu Gly Arg Met Glu Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu  
 275 280 285  
 Gly Ser Thr Gly Thr Ser Glu Ser Ser Val Glu Ala Arg Gly Ser Glu  
 290 295 300  
 Glu Val Arg Glu Ser Ser Thr Val Ala Ser Asp Gly Ser Met Glu Gly  
 305 310 315 320

A4  
 Cont

a4  
cont

<221> variation  
<222> (25)  
<223> Degenerated primers

<400> 3  
catcttcgtc gtcggcacng ynggnaa

27

<210> 4  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Primer

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<222> (21)  
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gggtggcaga tggccarrya nckytic

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<210> 5  
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<223> Modified base : 3'-deoxyadenosine

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ccatcctaatac gactcact atagggc

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<210> 7  
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actcactata gggctcgagc ggc

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<210> 8

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer

<400> 8

tttatcttta acctcctcgt caccgacc

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<210> 9

<211> 20

<212> DNA

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<400> 9

tagtggtgca gcgcaagccg

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<400> 10

ggcagcgttc cactgacacc aagacaatgg

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<212> DNA

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<210> 14  
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<210> 16  
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Sequence

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cacagaaagc ataaccagtg attgaacc

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<210> 17

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<210> 18

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 18

ttgtcaccag cataggcact gagtg

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